

In the Claims:

1. (Currently Amended) A method of diagnosing an iron disorder or a genetic susceptibility to developing said disorder in a mammal, comprising determining the presence of a mutation in exon 2 of ~~an~~ a histocompatibility iron loading (HFE) nucleic acid in a biological sample from said mammal, wherein said mutation is at position 193 of SEQ ID NO:1 and is not a C → G substitution at nucleotide 187 of SEQ ID NO:1 and wherein the presence of said mutation is indicative of said disorder or a genetic susceptibility to developing said disorder and wherein said determining step is carried out by nucleic acid hybridization on a microchip.

2. (Original) The method of claim 1, wherein said disorder is hemochromatosis.

3.-58. (Cancelled)

59. (Previously Presented) The method of claim 1, wherein said mutation at position 193 of SEQ ID NO:1 is an A → T substitution.

60. (Previously Presented) The method of claim 1, wherein said mutation at position 193 is determined by contacting said HFE nucleic acid with a nucleic acid sequence comprising the nucleotide sequence of SEQ ID NO:30.

61. (Previously Presented) The method of claim 1, wherein said mutation at position 193 is determined by contacting said HFE nucleic acid with a nucleic acid sequence comprising nucleotides 67-339 of SEQ ID NO:1.

62. (Previously Presented) The method of claim 1, wherein said mutation at position 193 is determined by contacting said HFE nucleic acid with a nucleic acid sequence comprising nucleotides 172-204 of SEQ ID NO:1.

63. (Previously Presented) The method of claim 1, wherein said mutation at position 193 is detected by contacting said HFE nucleic acid with a nucleic acid sequence comprising nucleotides 4652-4915 of SEQ ID NO:27.

64. (Previously Presented) The method of claim 1, further comprising determining the presence of a mutation in exon 4 at nucleotide 845 of SEQ ID NO:1.

65. (Previously Presented) The method of claim 64, wherein said mutation at position 845 is determined by contacting said HFE nucleic acid with a nucleic acid sequence comprising nucleotides 6494-6769 of SEQ ID NO:27.

66. (Previously Presented) The method of claim 1, further comprising determining the presence of a mutation in intron 4 at nucleotide 6884 of SEQ ID NO:27.

67. (Previously Presented) The method of claim 66, wherein said mutation at position 845 is determined by contacting said HFE nucleic acid with a nucleic acid sequence comprising nucleotides 6770-6927 of SEQ ID NO:27.